

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Lal, Preeti  
Corley, Neil C.  
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN RETICULOCALBIN ISOFORMS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Hereewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0358 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 328 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: RATRNOT02
  - (B) CLONE: 922578

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His
1				5					10					15	
Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly
			20					25					30		
Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala
		35					40					45			
His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val
	50					55					60				
Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu
65					70					75				80	
Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp
			85						90					95	
Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg
			100					105					110		
His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp	
	115						120				125				
Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly
	130					135					140				
His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr
145					150					155				160	
Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Phe	Arg	Val	Ala	Asp	
			165						170					175	
Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu
			180					185					190		
His	Pro	Glu	Glu	Phe	Pro	His	Met	Arg	Asp	Ile	Val	Ile	Ala	Glu	Thr
	195						200					205			
Leu	Glu	Asp	Leu	Asp	Arg	Asn	Lys	Asp	Gly	Tyr	Val	Gln	Val	Glu	Glu
	210					215					220				
Tyr	Ile	Ala	Asp	Leu	Tyr	Ser	Ala	Glu	Pro	Gly	Glu	Glu	Glu	Pro	Ala
225					230					235				240	
Trp	Val	Gln	Thr	Glu	Arg	Gln	Gln	Phe	Arg	Asp	Phe	Arg	Asp	Leu	Asn
			245						250					255	
Lys	Asp	Gly	His	Leu	Asp	Gly	Ser	Glu	Val	Gly	His	Trp	Val	Leu	Pro
			260					265					270		
Pro	Ala	Gln	Asp	Gln	Pro	Leu	Val	Glu	Ala	Asn	His	Leu	Leu	His	Glu
		275					280					285			
Ser	Asp	Thr	Asp	Lys	Asp	Gly	Arg	Leu	Ser	Lys	Ala	Glu	Ile	Leu	Gly
	290				295						300				
Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr	Gly	Glu	Asp
305				310						315				320	
Leu	Thr	Arg	His	His	Asp	Glu	Leu								
				325											

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: RATRNOT2
- (B) CLONE: 922578

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGCAGAGCGG	ACGTGGAGAG	CGGACGNCAG	CTGGATAACA	GGGGACCGAT	GATGTGGCGA	60
CCATCAGTTC	TGCTGCTTCT	GTTGCTACTG	AGGCACGGGG	CCCAGGGGAA	GCCATCCCCA	120

GACGCAGGCC	CTCATGGCCA	GGGGAGGGTG	CACCAGGCGG	CCCCCCTGAG	CGACGCTCCC	180
CATGATGACG	CCCACGGGAA	CTTCCAGTAC	GACCATGAGG	CTTTCCTGGG	ACGGGAAGTG	240
GCCAAGGAAT	TCGACCAACT	CACCCCAGAG	GAAAGCCAGG	CCCGTCTGGG	GCGGATCGTG	300
GACCGCATGG	ACCGCGCGGG	GGACGGCGAC	GGCTGGGTGT	CGCTGGCCGA	GCTTCGCGCG	360
TGGATCGCGC	ACACGCAGCA	GCGGCACATA	CGGGACTCGG	TGAGCGCGGC	CTGGGACACG	420
TACGACACGG	ACCGCGACGG	GCGTGTGGGT	TGGGAGGAGC	TGCGCAACGC	CACCTATGGC	480
CACTACGCGC	CCGGTGAAGA	ATTTTCATGAC	GTGGAGGATG	CAGAGACCTA	CAAAAAGATG	540
CTGGCTCGGG	ACGAGCGGCG	TTTCCGGGTG	GCCGACCAGG	ATGGGGACTC	GATGGCCACT	600
CGAGAGGAGC	TGACAGCCTT	CCTGCACCCC	GAGGAGTTCC	CTCACATGCG	GGACATCGTG	660
ATTGCTGAAA	CCCTGGAGGA	CCTGGACAGA	AACAAAGATG	GCTATGTCCA	GGTGGAGGAG	720
TACATCGCGG	ATCTGTACTC	AGCCGAGCCT	GGGGAGGAGG	AGCCGGCGTG	GGTGCAGACG	780
GAGAGGCAGC	AGTTCCGGGA	CTTCCGGGAT	CTGAACAAGG	ATGGGCACCT	GGATGGGAGT	840
GAGGTGGGCC	ACTGGGTGCT	GCCCCCTGCC	CAGGACCAGC	CCCTGGTGGA	AGCCAACCAC	900
CTGCTGCACG	AGAGCGACAC	GGACAAGGAT	GGGCGGCTGA	GCAAAGCGGA	AATCCTGGGT	960
AATTGGAACA	TGTTTGTGGG	CAGTCAGGCC	ACCAACTATG	GCGAGGACCT	GACCCGGCAC	1020
CACGATGAGC	TGTGAGCACC	GCGCACCTGC	CACAGCCTCA	GAGGCCCGCA	CAATGACCGG	1080
AGGAGGGGCC	GCTGTGGTCT	GGCCCCCTCC	CTGTCCAGGC	CCCGCAGGAG	GCAGATGCAG	1140
TCCAGGCAT	CCTCCTGCCC	CTGGGCTCTC	AGGGACCCCC	TGGGTCTGGCT	TCTGTCCCTG	1200
TCACACCCCC	AACCCAGGG	AGGGGCTGTC	ATAGTCCCAG	AGGATAAGCA	ATACCTATTT	1260
CTGACTGAGT	CTCCCAGCCC	AGACCCAGGG	ACCCTTGGCC	CCAAGCTCAG	CTCTAAGAAC	1320
CGCCCCAACC	CCTCCAGCTC	CAAATCTGAG	CCTCCACCAC	ATAGACTGAA	ACTCCCCTGG	1380
CCCCAGCCCT	CTCCTGCCTG	GCCTGGCCTG	GGACACCTCC	TCTCTGCCAG	GAGGCAATAA	1440
AAGCCAGCGC	CGGGAAAAAA	AAA				1463

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601793

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asp	Leu	Arg	Gln	Phe	Leu	Met	Cys	Leu	Ser	Leu	Cys	Thr	Ala	Phe
1				5				10						15	
Ala	Leu	Ser	Lys	Pro	Thr	Glu	Lys	Lys	Asp	Arg	Val	His	His	Glu	Pro
			20					25					30		
Gln	Leu	Ser	Asp	Lys	Val	His	Asn	Asp	Ala	Gln	Ser	Phe	Asp	Tyr	Asp
		35					40					45			
His	Asp	Ala	Phe	Leu	Gly	Ala	Glu	Glu	Ala	Lys	Thr	Phe	Asp	Gln	Leu
	50				55						60				
Thr	Pro	Glu	Glu	Ser	Lys	Glu	Arg	Leu	Gly	Lys	Ile	Val	Ser	Lys	Ile
65				70						75				80	
Asp	Gly	Asp	Lys	Asp	Gly	Phe	Val	Thr	Val	Asp	Glu	Leu	Lys	Asp	Trp
			85						90					95	
Ile	Lys	Phe	Ala	Gln	Lys	Arg	Trp	Ile	Tyr	Glu	Asp	Val	Glu	Arg	Gln
			100					105					110		
Trp	Lys	Gly	His	Asp	Leu	Asn	Glu	Asp	Gly	Leu	Val	Ser	Trp	Glu	Glu
		115				120						125			
Tyr	Lys	Asn	Ala	Thr	Tyr	Gly	Tyr	Val	Leu	Asp	Asp	Pro	Asp	Pro	Asp
	130					135					140				
Asp	Gly	Phe	Asn	Tyr	Lys	Gln	Met	Met	Val	Arg	Asp	Glu	Arg	Arg	Phe
145				150						155				160	
Lys	Met	Ala	Asp	Lys	Asp	Gly	Asp	Leu	Ile	Ala	Thr	Lys	Glu	Glu	Phe
			165					170						175	

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Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
      180      185      190
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
      195      200      205
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
      210      215      220
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
      225      230      235      240
Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Glu Thr Lys Asp
      245      250      255
Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
      260      265      270
Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
      275      280      285
Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
      290      295      300
Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
      305      310      315

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## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
- (B) CLONE: 1601793

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCCCGCTTCCG GTTGGGCGGT GCTTGCGCGC GTGAGCTGAG CCGGTGGGTG AGCGGCGGCC      60
ACGGCATCCT GTGCTGTGGG GGCTACGAGG AAAGATCTAA TTATCATGGA CCTGCGACAG      120
TTTCTTATGT GCCTGTCCCT GTGCACAGCC TTTGCCTTGA GCAAACCCAC AGAAAAGAAG      180
GACCGTGTAC ATCATGAGCC TCAGCTCAGT GACAAGGTTT ACAATGATGC TCAGAGTTTT      240
GATTATGACC ATGATGCCTT CTTGGGTGCT GAAGAAGCAA AGACCTTTGA TCAGCTGACA      300
CCAGAAGAGA GCAAGGAAAG GCTTGGAAAG ATTGTAAGTA AAATAGATGG CGACAAGGAC      360
GGGTTTGTCA CTGTGGATGA GCTCAAAGAC TGGATTAAAT TTGCACAAAA GCGCTGGATT      420
TACGAGGATG TAGACGACA GTGGAAGGGG CATGACCTCA ATGAGGACGG CCTCGTTTCC      480
TGGGAGGAGT ATAAAAATGC CACCTACGGC TACGTTTTAG ATGATCCAGA TCCTGATGAT      540
GGATTTAAC'T ATAAACAGAT GATGGTTAGA GATGAGCGGA GGTTTAAAT GGCAGACAAG      600
GATGGAGACC TCATTGCCAC CAAGGAGGAG TTCACAGCTT TCCTGCACCC TGAGGAGTAT      660
GACTACATGA AAGATATAGT AGTACAGGAA ACAATGGAAG ATATAGATAA GAATGCTGAT      720
GGTTTCATTG ATCTAGAAGA GTATATTGGT GACATGTACA GCCATGATGG GAATACTGAT      780
GAGCCAGAAAT GGGTAAAGAC AGAGCGAGAG CAGTTTGTG AGTTTCGGGA TAAGAACCGT      840
GATGGGAAGA TGGACAAGGA AGAGACCAAA GACTGGATCC TTCCCTCAGA CTATGATCAT      900
GCAGAGGCAG AAGCCAGGCA CCTGGTCTAT GAATCAGACC AAAACAAGGA TGGCAAGCTT      960
ACCAAGGAGG AGATCGTTGA CAAGTATGAC TTATTTGTG GCAGCCAGGC CACAGATTTT      1020
GGGGAGGCCT TAGTACGGCA TGATGAGTTC TGAGCTACGG AGGAACCCTC ATTTCTCAA      1080
AAGTAATTTA TTTTACAGC TTCTGGTTTC ACATGAAATT GTTTGCGCTA CTGAGACTGT      1140
TACTACAAAC TTTTAAAGAC ATGAAAAGGC GTAATGAAA CCATCCCGTC CCCATTCTCT      1200
CTCCTCTCTG AGGACTGGA GGAAGCCGT GCTTCTGAGG AACAACCTA ATTAGTACAC      1260
TTGTGTTTGT AGATTACAC TTTGTATTAT GTATTACAT GCGGTGTTTA TTTTGTATT      1320
TTTCTCTGGT TGGGAGTATG ATATGAAGGA TCAAGATCCT CAACTCACAC ATGTAGACAA      1380
ACATTAGCTC TTTACTCTTT CTCAACCCCT TTTATGATTT TAATAATTCT CACTTAACCTA      1440
ATTTTGTAAG CCTGAGATCA ATAAGAAATG TTCAGGAGAG AGGAAAGAAA AAAAATATAT      1500
GCTCCACAAT TTATATTTAG AGAGAGAACA CTTAGTCTTG CCTGTCAAAA AGTCCAACAT      1560
TTCATAGGTA GTAGGGGCCA CATATTACAT TCAGTTGCTA TAGGTCCAGC AACTGAACCT      1620
GCCATTACCT GGGCAAGGAA AGATCCCTTT GCTCTAGGAA AGCTTGGCCC AAATTGATTT      1680

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TCTTCTTTTT	CCCCCTGTAG	GACTGACTGT	TGGCTAATTT	TGTCAAGCAC	AGCTGTGGTG	1740
GGAAGAGTTA	GGGCCAGTGT	CTTGAAAATC	AATCAAGTAG	TGAATGTGAT	CTCTTTGCAG	1800
AGCTATAGAT	AGAAACAGCT	GGAAAACATA	AGGAAAAATA	CAAATGTTTT	CGGGGCATAC	1860
ATTTTTTTTC	TGGGTGTGCA	TCTGTTGAAA	TGCTCAAGAC	TTAATTATTT	GCCTTTTGAA	1920
ATCACTGTAA	ATGCCCCCAT	CCGGTTCCTC	TTCTTCCCAG	GTGTGCCAAG	GAATTAATCT	1980
TGGTTTCACT	ACAATTAAAA	TTCACCTCCT	TCCAATCATG	TCATTGAAAG	TGCCTTTAAC	2040
GAAAGAAATG	GTCACGTAAT	GGGAATTCTC	TTAAGAAACC	CTGAGATTAA	AAAAAGACTA	2100
TTTGGATAAC	TTATAGGAAA	GCCTAGAACC	TCCCAGTAGA	GTGGGGATTT	TTTTCTTCTT	2160
CCCTTTCCTT	TTTGGACAAT	AGTTAAATTA	GCAGTATTAG	TTATGAGTTT	GGTTGCAGTG	2220
TTCTTATCTT	GTGGGCTGAT	TTCCAAAAAC	CACATGCTGC	TGAATTTACC	AGGGATCCTC	2280
ATACCTCACA	ATGCAAACCA	CTTACTACCA	GGCCTTTTTT	TGTGTCCACT	GGAGAGCTTG	2340
AGCTCACACT	CAAAGATCAG	AGGACCTACA	GAGAGGGCTC	TTTGGTTTGA	GGACCATGGC	2400
TTACCTTTCC	TGCCTTTGAC	CCATCACACC	CCATTTCCCT	CTCTTTCCCT	CTCCCCGCTG	2460
CCAAAAAATA	AAAAAAGGA	AACGTTTATC	ATGAATCAAC	AGGGTTTCAG	TCCTTATCAA	2520
AGAGAGATGT	GGAAAGAGCT	AAAGAAACCA	CCCTTTGTTC	CCAACCTCCAC	TTTACCCATA	2580
TTTATGCAA	CACAAACACT	GTCCTTTTGG	GTCCCTTTCT	TACAGATGGG	ACCTCTTGAG	2640
GAAGGAATTA	TCGTATTC					2658

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1262329

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Arg	Gly	Gly	Arg	Gly	Arg	Arg	Leu	Gly	Leu	Ala	Leu	Gly	Leu
1				5					10					15	
Leu	Leu	Ala	Leu	Val	Leu	Ala	Pro	Arg	Val	Leu	Arg	Ala	Lys	Pro	Thr
			20					25					30		
Val	Arg	Lys	Glu	Arg	Val	Val	Arg	Pro	Asp	Ser	Glu	Leu	Gly	Glu	Arg
		35					40					45			
Pro	Pro	Glu	Asp	Asn	Gln	Ser	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu
	50					55				60					
Gly	Lys	Glu	Asp	Ser	Lys	Thr	Phe	Asp	Gln	Leu	Thr	Pro	Asp	Glu	Ser
65					70				75					80	
Lys	Glu	Arg	Leu	Gly	Lys	Ile	Val	Asp	Arg	Ile	Asp	Asn	Asp	Gly	Asp
			85					90					95		
Gly	Phe	Val	Thr	Thr	Glu	Glu	Leu	Lys	Thr	Trp	Ile	Lys	Arg	Val	Gln
		100					105					110			
Lys	Arg	Tyr	Ile	Phe	Asp	Asn	Val	Ala	Lys	Val	Trp	Lys	Asp	Tyr	Asp
	115					120					125				
Arg	Asp	Lys	Asp	Asp	Lys	Ile	Ser	Trp	Glu	Glu	Tyr	Lys	Gln	Ala	Thr
	130				135						140				
Tyr	Gly	Tyr	Tyr	Leu	Gly	Asn	Pro	Ala	Glu	Phe	His	Asp	Ser	Ser	Asp
145				150					155					160	
His	His	Thr	Phe	Lys	Met	Leu	Pro	Arg	Asp	Glu	Arg	Arg	Phe	Lys	
			165					170					175		
Ala	Ala	Asp	Leu	Asn	Gly	Asp	Leu	Thr	Ala	Thr	Arg	Glu	Glu	Phe	Thr
		180					185					190			
Ala	Phe	Leu	His	Pro	Glu	Glu	Phe	Glu	His	Met	Lys	Glu	Ile	Val	Val
	195					200					205				
Leu	Glu	Thr	Leu	Glu	Asp	Ile	Asp	Lys	Asn	Gly	Asp	Gly	Phe	Val	Asp
	210				215						220				

Gln	Asp	Glu	Tyr	Ile	Ala	Asp	Met	Phe	Ser	His	Glu	Glu	Asn	Gly	Pro
225					230					235					240
Glu	Pro	Asp	Trp	Val	Leu	Ser	Glu	Arg	Glu	Gln	Phe	Asn	Glu	Phe	Arg
				245					250					255	
Asp	Leu	Asn	Lys	Asp	Gly	Lys	Leu	Asp	Lys	Asp	Glu	Ile	Arg	His	Trp
		260					265					270			
Ile	Leu	Pro	Gln	Asp	Tyr	Asp	His	Ala	Gln	Ala	Glu	Ala	Arg	His	Leu
		275					280					285			
Val	Tyr	Glu	Ser	Asp	Lys	Asn	Lys	Asp	Glu	Lys	Leu	Thr	Lys	Glu	Glu
	290					295					300				
Ile	Leu	Glu	Asn	Trp	Asn	Met	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asn	Tyr
305				310						315					320
Gly	Glu	Asp	Leu	Thr	Lys	Asn	His	Asp	Glu	Leu					
				325						330					

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 780361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Arg	Asp	Val	Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser
1				5					10					15	
Gln	Ala	Arg	Leu	Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Leu	Ala	Gly	Asp
			20					25					30		
Ser	Asp	Gly	Trp	Val	Ser	Leu	Ala	Ala	Leu	Arg	Ala	Trp	Ile	Ala	His
		35				40						45			
Thr	Gln	Gln	Arg	His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	His	Thr
	50					55					60				
Tyr	Asp	Thr	Asp	Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn
65					70					75					80
Ala	Thr	Tyr	Gly	His	Tyr	Glu	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu
				85					90					95	
Gly	Pro														